



*Contributions of **BioMove members** at the 46th Annual Meeting of the Ecological Society of Germany, Austria and Switzerland (GfÖ)
Marburg, 05.-09. September 2016*

Session 3 - Biodiversity on the move: integrating movement ecology and biodiversity research

*Chairs: **Ulrike Schlägel, Antje Herde, Niels Blaum, Florian Jeltsch***

Biodiversity intrigues ecologists since decades. Long-standing efforts in both empirical and theoretical research aim to identify the mechanisms and environmental conditions that allow species to coexist and build diverse communities. In contrast, movement ecology has become a thriving field only recently thanks to modern tracking technology. Rapidly improving data collection and analysis methods allow us to follow organisms as they forage, disperse or migrate. This opens new dimensions for understanding not only movement processes themselves but also their role for biodiversity and ecosystem functioning. Mobility can facilitate niche differences, allowing individuals to segregate in space and time, or differences in movement abilities may trade off competitive (dis-) advantages. Additionally, animals that serve as mobile links transport seeds, pollen or other organisms, redistribute resources across habitats, or provide critical disturbance regimes.

One of our current challenges in ecology is to predict if and how species diversity is maintained under environmental changes due to climate change and human land-use. Habitat loss and fragmentation threaten diversity not only directly by reducing available habitat but also by impeding critical movement processes. At the same time, movement-mediated habitat connectivity may become key for the persistence of communities and ecosystems.

In this session, we bridge the gap between biodiversity research and movement ecology. In particular we invite theoretical, empirical and experimental studies that show how movement of organisms directly or indirectly impacts coexistence, community composition and dynamics, or species distributions. We also welcome studies that address how we can infer underlying movement processes from observed biodiversity patterns, and any other aspects on how movement and biodiversity interact in a changing world.

Session 3-O1

Movement-mediated biodiversity in a changing world

[Ulrike Schlägel](#)¹, [Antje Herde](#)¹, [Niels Blaum](#)¹, [Florian Jeltsch](#)¹, BioMove RTG Members^{1,2,3,4}

¹University of Potsdam, Institute of Biochemistry and Biology, Potsdam, DE, ulrike.schlaegel@gmail.com

²Freie Universität Berlin, Berlin, DE

³Leibniz Institute for Zoo and Wildlife Research, Berlin, DE

⁴Leibniz Centre for Agricultural Landscape Research, Müncheberg, DE

Biodiversity trends due to anthropogenic environmental change are varied. While we experience an overall loss of species, individual communities and metacommunities may increase or decrease in diversity, depending on spatial scale, landscape configuration and composition, and species interactions. Many of the processes that shape community composition and allow species coexistence are mediated by animal movement and in particular the movement of individuals, which have different motivations, vary in their strategies, and respond to differing local environments. Yet many existing theoretical approaches in biodiversity represent movement phenomenologically, e.g. by assuming basic dispersal kernels or space-use patterns. We present a framework for future research interfacing movement ecology and biodiversity research. Our framework merges concepts from movement ecology and coexistence theory and embeds them in community assembly. With this, we embrace an ongoing paradigm shift from a classical view that focuses on species' averages towards an individual-based perspective in biodiversity research.

Session 3-O2

Choosing the right tool for the job: Range vs. occurrence distributions for quantifying animal space use

[Justin Calabrese](#)^{1,2}, [Chris Fleming](#)^{1,2}

¹Smithsonian Institution, Front Royal, US, CalabreseJ@si.edu

²University of Maryland, College Park, US

Understanding animals' space requirements is a core goal of movement ecology and is a key reason for collecting relocation data. The amounts, types, and qualities of the various habitats an individual occupies will all influence its fitness.

Furthermore, as remaining natural areas decrease in size and become increasingly fragmented and disturbed, an understanding of species' space requirements is critical for designing effective conservation strategies. The importance of quantifying space use was recognized early in the development of ecology and has led to the concepts of "home range" and "utilization distribution". Space use, however, is a multifaceted aspect of animal behavior. Consequently, the home range concept has broadened substantially over time and a large and diverse literature on the subject now exists. This proliferation of concepts and methods has led to substantially different definitions of space use being conflated in the literature. To cut through this complexity, we show that many of these ideas cluster around two distinct notions of the utilization distribution. The range distribution describes the long-run behavior of a space-restricted movement process, and is consistent with the classical definition of home range. In contrast, the occurrence distribution quantifies uncertainty in the location of an individual during the observation period, can be used to link movement to

environmental covariates, and is not directly related to the classical notion of home range. Using mathematical arguments, simulated data, and an empirical example with African buffalo, we demonstrate that the range and occurrence distributions quantify fundamentally different aspects of animal space use. We then show the linkages between different space use estimators in the literature and these two distributions. Finally, we describe how these contrasting notions of space use can be used to answer different ecological questions.

Session 3-O3

How landscape diversity affects animals? Energy expenditure via movement

[Wiebke Ullmann](#)^{1,2}, Christina Fischer³, Karin Pirhofer-Walzl², [Niels Blaum](#)¹

¹University of Potsdam - Plant Ecology and Nature Conservation, Potsdam, DE

²Leibniz Center for Agricultural Landscape Research, Müncheberg, DE

³Technische Universität München - Ecology and Ecosystem Management, München, DE

Intensive agricultural land-use leads to the homogenization of structural landscape diversity, where a large matrix of fields surrounds small habitat remnants. In these agricultural landscapes with low structural diversity, animals often increase their home ranges to meet their nutritional and reproductive requirements. This response may result in higher energy expenditure for movement and less time for energy intake, which reduces individual fitness and may lead to a decline in animal abundance or even to the local extinction of a species. We selected the European hare (*Lepus europaeus*), often typical in agricultural landscapes, as our study species. Hare movements were recorded within two regions in Germany with pronounced differences in structural landscape diversity. In Bavaria, landscape diversity and hare abundances are high, whereas in Brandenburg, landscapes are homogenous and hare abundances are low. We were interested in understanding whether (1) hares in structurally diverse landscapes expend less energy than hares in homogenous landscapes, (2) larger home ranges result in higher energy expenditure, and (3) sudden resource changes (i.e. harvest) increase energy expenditure as hares search for alternative food sources. From 2011 to 2015 fifty hares were collared with GPS-tags including acceleration sensors. Acceleration data was used to calculate the overall dynamic body acceleration (ODBA) as a proxy for energy expenditure. Contrary to our predictions, energy expenditure decreased after sudden resource changes. However, energy expenditure increased significantly with home range size, but only for male hares. This effect was stronger for hares in diverse landscapes. Surprisingly, despite having significantly larger home ranges in homogenous landscapes, hares did not expend more energy than in diverse landscapes.

Session 3-O4

Spatial ecology of urban squirrels and hedgehogs

[James M. Turner](#)¹, Lisa Warnecke¹, Stephanie Reher¹, Anju M. Abel¹, Sandra Fischer¹, Elisabeth Gajare¹, Peer Gregersen¹, Annalena Stuhlmann¹, Edna Teich¹, Lea S. Thomas¹, Kathrin H. Dausmann¹

¹University of Hamburg, Hamburg, DE, james.turner@uni-hamburg.de

Urbanisation is a continually expanding, anthropogenic process that fragments and damages native habitat. Consequently, it is generally associated with negative effects such as population decreases and the local extirpation of native wildlife.

There are exceptions to this trend and although several species thrive in the urban environment we have little understanding of the underlying mechanisms contributing to their persistence. To quantify the effects of urbanisation on the spatial ecology of two species successfully inhabiting cities we examined the movement, foraging and activity patterns of the Eurasian red squirrel (*Sciurus vulgaris*) and European hedgehog (*Erinaceus europaeus*) in a large city in northern Germany using radio-telemetry. We found significant differences in home range size and core area use of squirrels among seasons and between urban and semi-natural habitat, which appeared to be largely influenced by food resource type and availability. Additionally, urban individuals' home ranges overlapped more than those in semi-natural habitat and they spent less time active. During their active season (May to November) hedgehogs had smaller home ranges than rural conspecifics, routinely crossed roads and preferred private gardens over parks for nesting and activity in the first part of the night. Our novel data illustrate how two small mammal species opportunistically adjust their movement ecology in response to immediate environmental conditions. The observed flexibility likely helps individuals maintain a positive energy balance and contributes to their success in habitat altered by urbanisation.

Session 3-05

Animal communities under environmental change: The role of traits and individual space use

[Lisa Teckentrup](#)¹, [Florian Jeltsch](#)¹

¹University of Potsdam, Potsdam, DE, lisa.teckentrup@uni-potsdam.de

Foraging movement and home range formation of individuals are key properties of animal communities since they determine their spatial structure and define the usage of resources within the environment. In face of environmental threats such as habitat loss, fragmentation or degradation animals alter their foraging movement and adapt their home ranges to the new conditions. These modifications in space use also affect community composition and structure. For a mechanistic understanding of community structures it is therefore crucial to identify key factors influencing individual space use and their effects on community composition and structure. In a previous modelling study which used an allometric model to simulate individual home range formation in animal communities, body mass was identified to determine the efficiency of different foraging strategies. We extend this modelling approach by introducing further traits such as different feeding types and habitat preferences that could act as key factors influencing foraging movement and affecting community structure. The model is then used to predict composition and structure of mammal communities in face of habitat loss, degradation and fragmentation for scenarios combining various foraging movement types and traits. Simulation results reveal how the different implemented traits influence community responses to environmental changes through modified foraging movement and habitat use. Thereby, this approach allows a mechanistic upscaling from individual organisms and traits to biodiversity pattern in heterogeneous landscapes.

Session 3-O6

From step selection function to utilization distribution: How best to make a pretty map

Johannes Signer¹, Tal Avgar³, John Fieberg²

¹Georg-August-Universität Göttingen, Göttingen, DE, jsigner@gwdg.de

²University of Minneapolis, St. Paul, US

³University of Alberta, Edmonton, CA

Ecologists have long been interested elucidating environmental drivers of animal movement and space-use patterns. Logistic regression models are often used to link environmental covariates to animal location data under the assumption that observations are statistically independent. Recent extensions allow joint modeling of animal movement and habitat selection via a conditional logistic regression modeling framework, thereby allowing researchers to take advantage of widespread availability of high resolution animal tracking data and hence dependent observations. These two analysis approaches are typically referred to as Resource Selection Analysis (RSA) and (integrated) Step Selection Analysis (SSA), respectively. The latter approach models conditional distributions – i.e., the likelihood is constructed for an observation at time t , conditional on the location at time $t-1$. This conditional formulation makes communicating results of SSA more challenging. In particular, managers often desire maps of expected utilization distributions (UD's), and it is not clear how these maps should be produced from fitted models. We explore two different approaches for generating maps from SSAs. First, we consider a naive approach that uses the coefficients from a fitted SSA model to estimate the UD, ignoring the conditional formulation of the model. Second, we consider a simulation-based approach, where space use is estimated by simulating movement via the fitted model. We compare the approaches using data generated by a stepping-stone process, where the underlying true UD is known. The simulation-based approach always provided better estimates of the true UD than the naive mapping approach. Differences between the approaches were greatest for complex landscapes and high sampling rates, suggesting that the simulation-based approach is likely to offer significant advantages when applying SSAs to real data.

Session 3-O7

Migration strength of hoverflies (*Syrphidae*) in relation to meteorological conditions

Lisa Fisler¹, Myles H. M. Menz¹

¹Institute of Ecology and Evolution, University of Bern, CH, isa.fisler@iee.unibe.ch

Hoverflies are known for their ecological services, such as aphid control and pollination, but little is known about their large-scale movements. Some species migrate south in large numbers during autumn, towards the Mediterranean. To understand more about these movements, we captured individuals with 2 m-high flight interception traps on an alpine pass in Switzerland. One trap was directed towards the South and the other towards the North, the latter capturing the majority of the animals. The results showed a higher abundance of insects flying towards the South against the wind rather than with tailwinds. The rain and the cold seemed to deter the hoverflies from flying, while peak movement was usually between 12:00 and 15:00 hrs. Also, for most of the species, few males in comparison to the females seemed to be undertaking

the journey. To our understanding, the insects have to adapt more to the weather conditions than bigger animals, due to their small size, and adopt different strategies to do so.

Session 3-O8

Understanding life-history strategies of migratory birds to study indirect impacts of global change on biodiversity

[Merlin Schaefer](#)^{1,2}, Stephan Menz², [Florian Jeltsch](#)², Damaris Zurell³

¹Leibniz Centre for Agricultural Landscape Research (ZALF), Müncheberg, DE, merlin.schaefer@uni-potsdam.de

²University of Potsdam, Potsdam, DE

³Swiss Federal Research Institute (WSL), Birmensdorf, CH

Migratory birds constitute an unneglectable part of avian biodiversity in seasonal environments. Due to their various interactions with other species, it is important to consider their temporal presence or absence, abundance and condition in biodiversity research. This requires a better understanding of their movement within an ecological and evolutionary context, especially since global change is increasingly affecting the behavioural patterns and population dynamics of migratory birds. Though recent advances in tracking technology helped in identifying current movement patterns of individuals, they lack the broader mechanistic perspective that is necessary for explaining migratory life-history strategies and for predicting anthropogenic impacts on the rhythmic movement pattern and population dynamics of migratory birds at the population level. Therefore, we implemented a flexible and soon freely available tool for modelling optimal animal life-history strategies in cyclic environments that is especially suited for theoretical studies of bird behaviour. In particular, we use stochastic dynamic programming to derive optimal state-based life-history strategies under cyclic food availability and wind conditions. Subsequently, we simulate population dynamics under the resulting strategy and potentially new environmental conditions. Here, we present the technique, the tool and exemplary results regarding potential impacts of global change on migratory birds, preparing the ground for further studies on how global change indirectly affects local biodiversity by changing movement patterns and population dynamics of migratory birds.

Session 3-O9

High-throughput movement ecology and its potential contribution to biodiversity and ecosystem research

[Ran Nathan](#)¹

¹Minerva Center for Movement Ecology, Hebrew University of Jerusalem, IL, ran.nathan@mail.huji.ac.il

The emerging field of movement ecology largely benefited from the recent development of new tracking technologies, enhanced computation abilities and powerful data analysis tools. Movement ecology studies have utilized those technological advances to better understand movement processes and predict movement patterns in general, and to examine how organismal movements affect biodiversity and ecosystem processes in particular. Despite these significant advances, some of the key questions in biodiversity and ecosystem research remain

unresolved due to the lack of data about movements of organisms at the scale and resolution relevant to the interactions between animals and their environment. In this talk I will introduce a new powerful tracking system that provides new opportunities for linking movement and biodiversity research at a regional scale (10-20 km wide). This high-throughput system, called ATLAS (Advanced Tracking and Localization of Animals in real-life Systems), has been developed over the last 3 years by the Minerva Center for Movement Ecology. The system is based on “reverse GPS” technology and is capable to automatically and simultaneously track multiple small animals in an area of 15x25 km, at high sampling frequency and GPS-level accuracy. We implemented the first prototype of this system at the Hula Valley (Israel) and our preliminary work has yielded a dataset of over 20 species and more than 300 million data points thus far. Combined with fine-resolution data on key landscape and ecosystem features, ATLAS-derived high-resolution multi-species movement data can be used to examine intra- and inter-specific interactions, as well as interactions between animals and their environment in unprecedented detail. Consequently, the ATLAS system could play a key role in enhancing our understanding of movement-biodiversity relationships, marking the onset of a big data era in movement ecology. This will allow re-examination of previous dogmas, conceptions and assumptions that have long underlied biodiversity research, and will also bring new challenges in managing and analyzing big data.

Session 3-O10

Linking animal movements with ecosystem functions

Thomas Mueller¹, Johanna Lenz¹, Katrin Böhning-Gaese¹

¹Senckenberg & Goethe Univ. Frankfurt, Frankfurt, DE, muellert@gmail.com

Spatially explicit mapping of ecosystem functions remains a challenge and methodological hurdles have limited our understanding of dispersal pathways on the landscape scale. We demonstrate how movement data of frugivores can be used for spatially explicit mapping of seed dispersal networks in fragmented landscapes. We combined movement data of 30 Trumpeter Hornbills (*Bycanistes bucinator*) with gut-passage times and high-resolution habitat data in a fragmented forest landscape in South Africa. We identified potential seed dispersal paths and distinguished whether potential seed transport happened between forest patches, within the same patch, or into the habitat matrix. To quantify functional landscape connectivity we identified all possible between-patch connections and used graph networks to estimate landscape connectivity provided by hornbills. Although potential between-patch dispersal events were rare (on average 7% of all dispersal paths), hornbills could cover distances of up to 15 km. Hornbills visited over 100 forest patches and connected a habitat network with an extent of about 50 km which increased the potential functional connectivity of the landscape more than two-fold. We identified habitat patches that were critical stepping stones for seed dispersal pathways. Without these stepping-stones the network would likely disintegrate into separated components and lead to isolation of forest fragments. We showed that large frugivorous birds can greatly improve functional connectivity for fleshy-fruited plants across broad scales. Combining high-resolution movement and landscape data into graph networks allows the identification of seed dispersal pathways and critical stepping stones in fragmented landscapes, which could be widely incorporated in reserve design and landscape-level conservation planning.

Session 3-O12

**Individual movement decisions shape disease dynamics:
Combining movement ecology and epidemiological models**

[Cédric Scherer](#)¹, [Viktoriia Radchuk](#)¹, [Niels Blaum](#)², [Volker Grimm](#)³, [Florian Jeltsch](#)²,
[Stephanie Kramer-Schadt](#)¹

¹Leibniz Institute for Zoo and Wildlife Research (IZW), Berlin, DE,
scherer@izw-berlin.de

²Universität Potsdam, Potsdam, DE

³Helmholtz Centre for Environmental Research (UFZ), Leipzig, DE

Host movement and thus individual movement decisions play an important role in driving on-going disease dynamics by transmitting pathogens to distant hosts, thereby connecting infected host patches with new areas that would otherwise be isolated. Thus, Riley et al. (2015) highlight the need to incorporate more flexible and accurate movement algorithms as well as spatially heterogeneous landscapes in disease models to overcome population-based assumptions and integrate landscape structure between patches. Examples for such movement assumptions are rare long-distance dispersal events versus small-scale exploring trips, avoidance of open fields and/or urban areas, changes in movement behavior due to infection, seasonal aggregations on so-called transmission islands, or variation in the perceptual range of the individuals. The aim of this modeling study is to expand existing disease models by including more realistic movement algorithms than the assumptions used before, such as reaction-diffusion, displacement rules, neighborhood infection, or random walks. We investigate well-established spatially-explicit individual-based disease models: SwifCoIBM which simulates classical swine fever (CSF) in its social host, the wild boar (*Sus scrofa*; SIR epidemiological system) and a model on the spread of rabies in foxes (*Vulpes vulpes*; SI epidemiological system). Using a set of homogeneous and heterogeneous landscape scenarios, we will compare the effect of increasing complex movement assumptions on disease persistence while varying spatial and temporal landscape heterogeneity. With our modeling approach we aim to contribute to understanding complex disease dynamics and host-pathogen coexistence by unravelling the mechanisms behind heterogeneity in host behavior and contact processes acting at different spatial and temporal scale.

Session 11 – Spatial patterns and ecological processes

Session 11-P7

In field distribution of phytopathogenic fungi of wheat - an analysis

[Gabriele Schiro](#)¹, [Marina Müller](#)¹, [Thomas Müller](#)¹

¹Leibniz Centre for Agricultural Landscape Research, Müncheberg, DE,
schiro@zalf.de

Filamentous fungi colonise the phyllosphere of wheat (*Triticum* spp.) They are often responsible for plant diseases causing severe yield losses and potential health problems for the consumers. We focus on phytopathogenic fungi belonging to two distinct genera, *Fusarium* spp. and *Alternaria* spp., found on the ear, the grain-bearing tip of the plant. *Fusarium* fungi are considered the responsible for the appearance of the “*Fusarium* head blight”, one of the most devastating diseases in wheat, while

Alternaria is responsible for a disease called “black dots”. Both genera produce mycotoxins that are toxic for consumers, once ingested. In this work, we determine the in-field distribution of these filamentous fungi, with the aim of explaining possible spatial patterns using in-field microclimatic conditions and biotic variables as proxies. Two wheat fields situated in the north part of Brandenburg are analysed. These fields have a hilly heterogeneous topography, which produces different microclimatic conditions, leading to a potential different microhabitat differentiation that could result in different species compositions. Among the biotic variables, a focus is given to the presence of bacteria belonging to the phylum of *Pseudomonas fluorescens*. Members of this phylum were, in the past, often found on the ears and showed a strong antagonism to phytopathogenic fungi. With our results, combined with in-vitro observations, we want to reach a better understanding of the dynamics of the microbial communities in the phyllosphere of wheat while setting the basis for the study of the dispersal processes that generate these patterns. The final aim is to provide useful information for the development of more sustainable plant-disease control methods.